



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application No.: 09/868,987

Applicant: MURDIN, Andrew D. et al.

Filed: December 23, 1999

TC/A.U.: 1645

Examiner: Padmavathi Baskar

Docket No: 032931/0253

DECLARATION PURSUANT TO 37 CFR 1.131

I, Andrew Murdin, Director, External R&D Canada, Aventis Pasteur, hereby declare that:

1. I am an inventor in the above-identified application, and am employed by the assignee, Aventis Pasteur.

2. Details of my employment history are as follows:

Since 2002 Director, External R&D Canada, Aventis Pasteur.

1999-2002 Principal Research Scientist, Aventis Pasteur.

1997-2002 Section Head, Aventis Pasteur.

1993-2003 Project Leader (Chlamydia), Aventis Pasteur.

1990-1993 Research Scientist, Connaught Laboratories Ltd. (subsequently Pasteur Merieux Connaught, subsequently Aventis Pasteur), Toronto, Canada.

1988-1990 Post-Doctoral Research Associate, Dept. of Microbiology, State University of New York, Stony Brook, NY, USA.

1985-1987 Post-Doctoral Research Fellow, Dept. of Microbiology, University of Surrey, Guildford, Surrey, England.

1981-1985 Scientific Officer, Vaccine Research Dept., Animal Virus Research Institute, Pirbright, Surrey, England.

Details of my education are as follows:


B.Sc., University of Bath, England, 1980

Ph.D., University of Surrey, England, 1986.

3. Attached is a copy of a document signed by me and Dathao Ho, an employee of the assignee Aventis Pasteur. The document sets forth the amino acid sequence, the nucleotide sequence, and the restriction map of CPN100686.
4. CPN100686 corresponds to the gene identified as SEQ ID Nos: 1 and 14 of the application. The amino acid sequence of CPN100686 set forth in the attached document is identical to SEQ ID No:14 of this application. The sequences and restriction map set forth in the document are essentially the same as those shown in Figures 1 and 14 of this application.
5. The dates deleted from the attached document are before November 4, 1998.
6. The document shows that I possessed these amino acid and nucleotide sequences prior to November 4, 1998.
7. I hereby declare that all statements made herein of my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issuing thereon.

Mord 6th 2504

Date



Andrew Murdin

Director, External R&D Canada, Aventis Pasteur

CONFIDENTIAL

>CPN100686 protein-export membrane protein SecD
VSSPILNVPLKNHASVSGKFTHREVSKLASDLKSGAMSFVPEVLSEETISSDLGKKQCTQGIISACCGLAMLIVL
MSVYYRFGGVIASGAVLLNLLLIWAALQYLDAPLTL SGLAGIVLAMGMAVDANVLVFERIREEFLLS QSLKKSVE
KGYTKAFGAIFDSNLTTVLASALLFFLDTGPIKGFALTILGIFSSMFTALFMTKFFFMLWMNKTQHTQLHMMNK
FVGIKHDFLRGCKKLWAVSGSVFLLGCVALGFGAWNSVLGMDFKGGYAFTFNPK EHGISDVAQM RGKV VHKLQEA
GLSSRDFRIQTFGSSEKIKIYFSDKSF KLYXSRYEPLSXNXRSXAGVNVGLLSETGLDFSTETLNETQNFWSKVS
SKLSKKMRYQATIGLLGALAIILLYVSLRFEWQYAFSAVCALIHDL LATCAVLFI AHFFLKKIQIDLQAIGALMT
VLGYSLNNTLIIFDRIREDRQANLFTPMHVLVNDALQKTF SRTVMTTATTL SVLLMLLFIGGSSVFNF AFI MTIG
ILLGTLS SLYIAPPLL

ACTUAL ENCODED SEQUENCE

1 MVSSPILNVP LKNHASVSGK FTHREVSKLA SDLKSGAMSF VPEVLSEETI
51 SSDLGKKQCT QCIISACCCL AMLIVLMSVY YRFGGVIASG AVLLNLLLIW
101 AALQYLDAPL TSLGLAGIVL AMGMAVDANV LVFERIREEF LLSQSLKKS
151 EKG YTKAFGA IFDSNLTTVL ASALLFFLDT GPIKGFALT ILGIFSSMFT
201 ALFMTKFFFM LWMNKTQHTQ LHMMNKFVGI KHDFLRGCKK LWAVSGSVFL
251 LGCV ALGFGA WNSVLGMDFK GGYAFTFNPK EHGISDVAQM RGKV VHKLQE
301 AGLSSRDFRI QTFGSSEKIK IYFSDKALSY TKQIRASLLK LTIMSWRYCG
351 I VVRNRPRFL YGNSKRNAKF WSKVSSKLSK KMRYQATIGL LGALAIILLY
401 VSLRFEWQYA FSAVCALIHDL LATCAVLFI AHFFLKKIQI DLQAIGALMT
451 VLGYSLNNTL IIFDRIREDR QANLFTPMHV LVNDALQKTF SRTVMTTAT
501 LSVLLMLLFI GGSSVFNF AFI MTIGILLGT LSSLYIAPPL LLFMVRKENR
551 SK*

CODING SEQUENCE

THE PROTEIN IS ENCODED ON THE POSITIVE STRAND

The ATG is presumably the start codon

The TAA is presumably the stop codon

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1  ATGGACTTCC GCATATTGTC AGGAGGGGAT CAGCGGCACT GCTAATGGAC
51  AATATTCTGC AAACCGTGGA TGGCGTATGG CTGTAGTGAT TGACGGTTAT
101 ATGGTCAGCA GCCCTATTTT AAACGTCCCA TTGAAAAATC ATGCCAGTGT
151 CTCAGGGAAT TTTACCCACC GTGAAGTGAG CAAACTCGCC TCAGATTTAA
201 AATCTGGAGC GATGTCTTTT GTTCCCGAGG TTCTCAGTGA AGAGACGATC
251 TCTTCTGATC TTGGGAAAAA ACAATGTACA CAAGGCATTA TCTCAGCATG
301 CTGTGGCTTG GCAATGCTTA TTGTTTTGAT GAGCGTATAT TATAGATTTG
351 GAGGCGTCAT CGCTTCGGGA GCTGTTCTTC TGAATCTTTT GCTTATCTGG
401 GCAGCTCTAC AGTATTTGGA TGCGCCACTC ACCTTGTCAG GACTCGCTGG
451 GATTGTTCTT GCTATGGGGA TGGCCGTAGA TGCAAATGTT CTTGTATTCG
501 AAAGAATCCG AGAGGAATTT TTATTGTCTC AAAGTCTTAA AAAATCTGTA
551 GAAAAAGGAT ATACCAAGGC TTTTGAGGCC ATTTTGGATT CTAAGTTGAC
601 TACAGTATTG GCCTCAGCAC TTCTTTTCTT CCTAGATACA GGGCCTATTA
651 AAGGGTTTGC TTTGACATTG ATTTTAGGAA TTTTCTCTTC AATGTTTACG
701 GCTCTTTTCA TGAATAAATT TTTCTTCATG CTGTGGATGA ATAAGACCCA
751 ACATACACAG TTGCATATGA TGAATAAGTT CGTGGGGATA AAGCATGATT
801 TCTTGAGAGG ATGCAAAAAA CTTTGGGCTG TTTCTGGAAG TGTTTTTCTT
851 TTAGGTTGCG TTGCTCTCGG GTTTGAGGCC TGAATTCCTG TTTTGGGAAT
901 GGATTTTAAA GGAGGGTATG CCTTTACCTT TAATCCAAAA GAGCATGGCA
951 TCAGCGATGT TGCTCAAATG CGTGGCAAAG TTGTGCATAA ACTACAGGAA
1001 GCTGGTCTTT CTTCTAGAGA CTTCCGTATT CAAACATTTG GATCTTCAGA
1051 AAAGATCAAA ATCTATTTTA GTGATAAAGC TTTAAGCTAT ACTAAGCAGA
1101 TACGAGCCTC TCTCCTAAAA TTAACGATCA TGAGCTGGCG TTATTGTGGG
1151 ATTGTTGTCA GAAACAGGCC TAGATTTCTC TACGGAAACT CTAAACGAAA
1201 CGCAAAATTT TGGTCAAAGG TAAGCAGCAA ACTATCGAAG AAAATGCGTT
1251 ATCAGGCGAC CATCGGGCTT TTAGGAGCTT TGGCAATCAT CTTGCTCTAT
1301 GTGAGTTTGC GCTTTGAATG GCAATATGCT TTCAGTGCCG TATGCGCTTT
1351 AATTCATGAC CTTTGGCTA CCTGTGCAGT CTTGTTTATA GCACATTTCT
1401 TTTTGAAGAA AATTCAAATA GATTTGCAAG CCATTGGTGC TTTAATGACT
1451 GTATTGGGGT ATTCATTAAA CAATACTTTG ATCATTTTGG ATCGTATTCG

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1501 TGAAGATCGC CAAGCGAACC TGTTTACCCC TATGCATGTT TTAGTTAATG
1551 ATGCCCTTCA AAAGACGTTC AGCCGCACGG TAATGACAAC AGCTACAAC
1601 CTATCAGTTT TGTTAATGCT TTTGTTTATA GGCGGCTCCT CTGTCTTTAA
1651 TTTTGCATTT ATTATGACCA TAGGGATTCT TCTAGGAAC TATCGTCTC
1701 TTTATATTGC ACCACCTCTG TTGTTGTTTA TGGTCCGTAA AGAAAATCGC
1751 TCAAAATAAG TACCGTTAAA CTTAATCTAA CGTGTAGCAA TATAAAAATC
1801 TCCTTTGGGA CTTTAGTCCC AAAGGCCCT GTGGTATTAA ATTTATGACA
1851 AATTCAGATA ATGC

SEQUENCE ALIGNMENT

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101 ATGGTCAGCAGCCCTATTTTAAACGTCCCATTGAAAAATCATGCCAGTGT 150
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    1 MetValSerSerProIleLeuAsnValProLeuLysAsnHisAlaSerVa 17

151 CTCAGGGAAATTTACCCACCGTGAAGTGAGCAAACCTCGCCTCAGATTTAA 200
    |||||||
    18 lSerGlyLysPheThrHisArgGluValSerLysLeuAlaSerAspLeuL 34

201 AATCTGGAGCGATGTCTTTTGTCTCCGAGGTTCTCAGTGAAGAGACGATC 250
    |||||||
    35 ysSerGlyAlaMetSerPheValProGluValLeuSerGluGluThrIle 50

251 TCTTCTGATCTTGGGAAAAACAATGTACACAAGGCATTATCTCAGCATG 300
    |||||||
    51 SerSerAspLeuGlyLysLysGlnCysThrGlnGlyIleIleSerAlaCy 67

301 CTGTGGCTTGGCAATGCTTATTTGTTTGTATGAGCGTATATTTATAGATTTG 350
    |||||||
    68 sCysGlyLeuAlaMetLeuIleValLeuMetSerValTyrTyrArgPheG 84

351 GAGGCGTCATCGCTTCGGGAGCTGTTCTTCTGAATCTTTTGCTTATCTGG 400
    |||||||
    85 lyGlyValIleAlaSerGlyAlaValLeuLeuAsnLeuLeuLeuIleTrp 100

401 GCAGCTCTACAGTATTTGGATGCGCCACTCACCTTGTCAGGACTCGCTGG 450
    |||||||
    101 AlaAlaLeuGlnTyrLeuAspAlaProLeuThrLeuSerGlyLeuAlaGl 117

451 GATTGTTCTTGCTATGGGGATGGCCGTAGATGCAAATGTTCTTGTATTTCG 500
    |||||||
    118 yIleValLeuAlaMetGlyMetAlaValAspAlaAsnValLeuValPheG 134

501 AAAGAATCCGAGAGGAATTTTATTGTCTCAAAGTCTTAAAAAATCTGTA 550
    |||||||
    135 luArgIleArgGluGluPheLeuLeuSerGlnSerLeuLysLysSerVal 150

551 GAAAAAGGATATACCAAGGCTTTTGGAGCCATTTTGTATTCTAACTTGAC 600
    |||||||
    151 GluLysGlyTyrThrLysAlaPheGlyAlaIlePheAspSerAsnLeuTh 167

601 TACAGTATTGGCCTCAGCACTTCTTTTCTTCTTAGATACAGGGCCTATTA 650
    |||||||
    168 rThrValLeuAlaSerAlaLeuLeuPhePheLeuAspThrGlyProIleL 184

651 AAGGGTTTGCTTTGACATTGATTTTAGGAATTTCTCTTCAATGTTTACG 700
    |||||||
    185 ysGlyPheAlaLeuThrLeuIleLeuGlyIlePheSerSerMetPheThr 200

701 GCTCTTTTCATGACTAAATTTTCTTCATGCTGTGGATGAATAAGACCCA 750
    |||||||
    201 AlaLeuPheMetThrLysPhePhePheMetLeuTrpMetAsnLysThrGl 217

751 ACATACACAGTTGCATATGATGAATAAGTTCGTGGGGATAAAGCATGATT 800
    |||||||
    218 nHisThrGlnLeuHisMetMetAsnLysPheValGlyIleLysHisAspP 234

801 TCTTGAGAGGATGCAAAAAAAGCTTTGGGCTGTTTCTGGAAGTGTTTTCTT 850
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    235 heLeuArgGlyCysLysLysLeuTrpAlaValSerGlySerValPheLeu 250

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251 LeuGlyCysValAlaLeuGlyPheGlyAlaTrpAsnSerValLeuGlyMe 267
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901 GGATTTTAAAGGAGGGTATGCCTTTACCTTTAATCCAAAAGAGCATGGCA 950
|||||
268 tAspPheLysGlyGlyTyrAlaPheThrPheAsnProLysGluHisGlyI 284
|||||
951 TCAGCGATGTTGCTCAAATGCGTGGCAAAGTTGTGCATAAACTACAGGAA 1000
|||||
285 leSerAspValAlaGlnMetArgGlyLysValValHisLysLeuGlnGlu 300
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1001 GCTGGTCTTTCCTCTAGAGACTTCCGTATTCAAACATTTGGATCTTCAGA 1050
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301 AlaGlyLeuSerSerArgAspPheArgIleGlnThrPheGlySerSerGl 317
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1051 AAAGATCAAAATCTATTTTAGTGATAAAGCTTTAAGCTATACTAAGCAGA 1100
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318 uLysIleLysIleTyrPheSerAspLysAlaLeuSerTyrThrLysGlnI 334
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335 leArgAlaSerLeuLeuLysLeuThrIleMetSerTrpArgTyrCysGly 350
|||||
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|||||
351 ileValValArgAsnArgProArgPheLeuTyrGlyAsnSerLysArgAs 367
|||||
1201 CGCAAAATTTTGGTCAAAGGTAAGCAGCAAACATATCGAAGAAAATGCGTT 1250
|||||
368 nAlaLysPheTrpSerLysValSerSerLysLeuSerLysLysMetArgT 384
|||||
1251 ATCAGGCGACCATCGGGCTTTTAGGAGCTTTGGCAATCATCTTGCTCTAT 1300
|||||
385 yrGlnAlaThrIleGlyLeuLeuGlyAlaLeuAlaIleIleLeuLeuTyr 400
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1301 GTGAGTTTGCCTTTGAATGGCAATATGCTTTTCAGTGCCGTATGCGCTTT 1350
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401 ValSerLeuArgPheGluTrpGlnTyrAlaPheSerAlaValCysAlaLe 417
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1351 AATTCATGACCTTTTGGCTACCTGTGCAGTCTTGTTTATAGCACATTTCT 1400
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418 uIleHisAspLeuLeuAlaThrCysAlaValLeuPheIleAlaHisPheP 434
|||||
1401 TTTTGAAGAAAATTCAAATAGATTTGCAAGCCATTGGTGCTTTAATGACT 1450
|||||
435 heLeuLysLysIleGlnIleAspLeuGlnAlaIleGlyAlaLeuMetThr 450
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1451 GTATTGGGGTATTCATTAAACAATACTTTGATCATTTTTGATCGTATTTCG 1500
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451 ValLeuGlyTyrSerLeuAsnAsnThrLeuIleIlePheAspArgIleAr 467
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1501 TGAAGATCGCCAAGCGAACCTGTTTACCCCTATGCATGTTTTAGTTAATG 1550
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468 gGluAspArgGlnAlaAsnLeuPheThrProMetHisValLeuValAsnA 484
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485 spAlaLeuGlnLysThrPheSerArgThrValMetThrThrAlaThrThr 500
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1601 CTATCAGTTTTGTTAATGCTTTTGTATTATAGGCGGCTCCTCTGTCTTTAA 1650
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501 LeuSerValLeuLeuMetLeuLeuPheIleGlyGlySerSerValPheAs 517

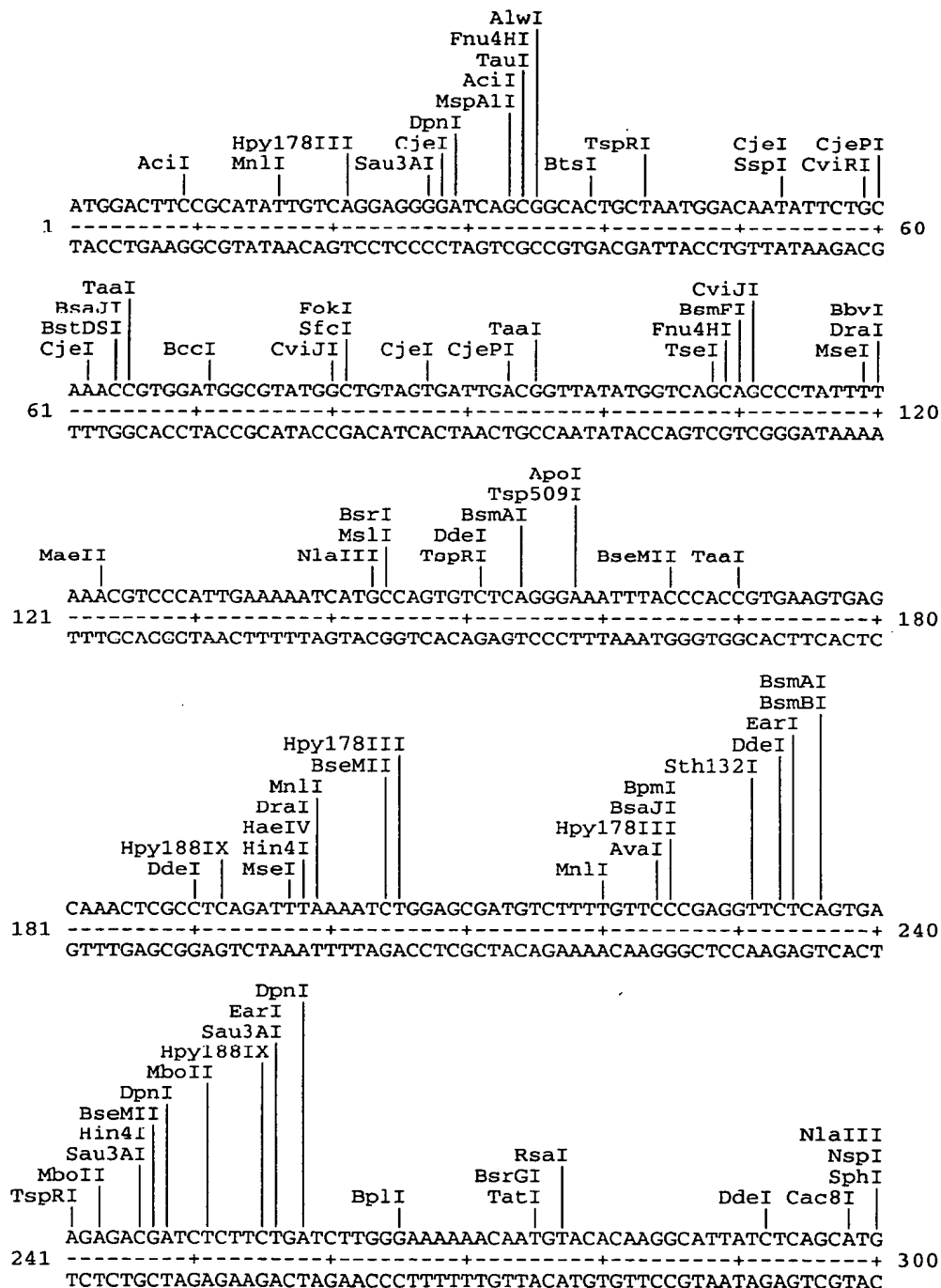
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1651 TTTTGCATTTATTATGACCATAGGGATTCTTCTAGGAACTTTATCGTCTC 1700
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518 nPheAlaPheIleMetThrIleGlyIleLeuLeuGlyThrLeuSerSerL 534
1701 TTTATATTGCACCACCTCTGTTGTTGTTTATGGTCCGTAAAGAAAATCGC 1750
|||||
535 euTyrIleAlaProProLeuLeuLeuPheMetValArgLysGluAsnArg 550
1751 TCAAAA 1756
|||||
551 SerLys 552

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RESTRICTION MAP



BseMII
 CviJI
 BsrDI
 MnlI
 HgaI
 AceIII
 Sth132I
 Hin4I
 BsaHI

301 CTGTGGCTTGGCAATGCTTATTGTTTTGATGAGCGTATATTATAGATTGGAGGCGTCAT
 -----+-----+-----+-----+-----+ 360
 GACACCGAACCCTTACGAATAACAAACTACTCGCATATAATATCTAAACCTCCGCAGTA

AceIII
 BbvI
 TaaI
 SfaNI
 SfcI
 AluI
 CviJI
 Fnu4HI
 TseI
 CjeI
 HinfI
 TfiI
 Hpy188IX
 Hpy178III
 MboII
 MwoI

361 CGCTTCGGGAGCTGTTCTTCTGAATCTTTTGCTTATCTGGGCAGCTCTACAGTATTTGGA
 -----+-----+-----+-----+-----+ 420
 GCGAAGCCCTCGACAAGAAGACTTAGAAAACGAATAGACCCGTCGAGATGTCATAAACCT

CviJI
 HaeIII
 BccI
 EaeI
 GdiII
 SfaNI
 BcefI
 HhaI
 HphI
 FokI
 CjeI
 Hpy178III
 PleI
 HinfI

421 TGCGCCACTCACCTTGTCAGGACTCGCTGGGATTGTTCTTGCTATGGGGA'GGCCGTAGA
 -----+-----+-----+-----+-----+ 480
 ACGCGGTGAGTGGAACAGTCCTGAGCGACCCTAACAAAGACGATACCCCTACCGGCATCT

Hpy188IX
 MnlI
 ApoI
 Tsp509I
 BsmAI
 MseI
 NspV
 HinfI
 TfiI
 CviRI
 FokI

481 TGCAAATGTTCTTGTATTTCGAAAGAATCCGAGAGGAATTTTATTGTCTCAAAGTCTTAA
 -----+-----+-----+-----+-----+ 540
 ACGTTTACAAGAACATAAGCTTTCTTAGGCTCTCCTTAAAAATAACAGAGTTTCAGAATT

CviJI
 BsaJI
 StyI
 CviJI
 NlaIV
 MwoI
 HinfI
 TfiI
 SfcI

541 AAAATCTGTAGAAAAAGGATATACCAAGGCTTTTGGAGCCATTTTGTATTCTAACTTGAC
 -----+-----+-----+-----+-----+ 600
 TTTTAGACATCTTTTCTATATGGTTCCGAAAACCTCGGTAAAACTAAGATTGAACTG

BbvCI
 Bpu10I
 DdeI
 CviJI
 HaeI
 TaaI
 HaeIII
 MboII
 MnlI
 BseMII
 BfaI
 EcoO109I
 Sau96I
 CviJI
 HaeIII
 EcoNI
 MseI
 BslI

601 TACAGTATTGGCCTCAGCACTTCTTTCTTCTTAGATACAGGGCCTATTAAAGGGTTTGC
 -----+-----+-----+-----+-----+ 660
 ATGTCATAACCGGAGTCGTGAAGAAAAGAAGGATCTATGTCCCGGATAATTTCCTCAAACG

ApoI
 Tsp509I
 MboII
 BceII
 NlaIII
 Hpy178III
 RcaI
 CviJI
 EarI
 ApoI
 MboII
 Tsp509I
 TTTGACATTGATTTTAGGAATTTTCTCTTCAATGTTTACGGCTCTTTTCATGACTAAATT
 661 ----- 720
 AAAGTGTAACTAAAATCCTTAAAGAGAAGTTACAAATGCCGAGAAAAGTACTGATTTAA

NdeI
 CviRI
 TaaI
 SimI
 FokI
 NlaIII
 XmnI
 TTTCTTCATGCTGTGGATGAATAAGACCCAACATACACAGTTGCATATGATCAATAAGTT
 721 ----- 780
 AAAGAAGTACGACACCTACTTATTCTGGGTTGTATGTGTCAACGTATACTACTTATTCAA

Hpy178III
 SmlI
 MnlI
 SfaNI
 NlaIII
 CviRI
 Bce83I
 FokI
 CviJI
 Hpy178III
 CGTGGGGATAAAGCATGATTTCTTGAGAGGATGCAAAAACTTTGGGCTGTTTCTGGAAG
 781 ----- 840
 GCACCCCTATTTTCGTACTAAAGAACTCTCCTACGTTTTTTTGAACCCGACAAAGACCTTC

ApoI
 EcoRI
 Tsp509I
 ScrFI
 CviJI
 EcoRII
 NlaIV
 Sth132I
 AvaI
 TGTTTTTCTTTTAGGTTGCGTTGCTCTCGGGTTTGGAGCCTGGAATTCCGTTTTGGGAAT
 841 ----- 900
 ACAAAAAGAAAATCCAACGCAACGAGAGCCCAACCTCGGACCTTAAGGCAAAACCTTA

DraI
 MseI
 MnlI
 MseI
 NlaIII
 SfaNI
 GGATTTTAAAGGAGGGTATGCCTTTACCTTTAATCCAAAAGAGCATGGCATCAGCGATGT
 901 ----- 960
 CCTAAAAATTCTCTCCATACGGAATGGAATTAGGTTTTCTCGTACCGTAGTCGCTACA

Hpy178III
 BfaI
 XbaI
 BsmAI
 MboII
 AluI
 CviJI
 SfcI
 CviRI
 TGCTCAAATGCGTGGCAAAGTTGTGCATAAACTACAGGAAGCTGGTCTTTCTTTCTAGAGA
 961 ----- 1020
 ACGAGTTTACGCACCGTTTCAACACGTATTTGATGTCCTTCGACCAGAAAGAAGATCTCT

BsaBI
 DpnI
 Sau3AI
 AlwI
 Hpy188IX

Tth111III
 DpnI
 BstYI
 Sau3AI
 Eco57I MboII
 HindIII
 AluI
 CviJI
 1021 CTTCCGTATTCAAACATTTGGATCTTCAGAAAAGATCAAAATCTATTTTAGTGATAAAGC 1080
 -----+-----+-----+-----+-----+
 GAAGGCATAAGTTTGTAACCTAGAAGTCTTTTCTAGTTTATAGATAAAATCACTATTTCG

Cac8I
 RleAI
 AluI
 CviJI
 NlaIII
 Hpy178III
 RcaI
 BplI
 DpnI
 Sau3AI
 MseI
 AceIII
 Tsp509I
 MnlI
 Hin4I
 CviJI
 DdeI
 AluI
 CviJI
 MseI
 1081 TTTAAGCTATACTAAGCAGATACGAGCCTCTCTCCTAAAATTAACGATCATGAGCTGGCG 1140
 -----+-----+-----+-----+-----+
 AAATTCGATATGATTTCGTCTATGCTCGGAGAGAGGATTTTAATTGCTAGTACTCGACCGC

BfaI
 CviJI
 HaeI
 HaeIII
 StuI
 Hpy188IX
 1141 TTATTGTGGGATTGTTGTCTAGAAACAGGCCTAGATTTCTCTACGGAACTCTAAACGAAA 1200
 -----+-----+-----+-----+-----+
 AATTACACCCTAACAACAGTCTTTGTCCGATCTAAAGAGATGCCTTTGAGATTTGCTTT

BcgI
 Fnu4HI
 TseI
 BbvI
 TaqI
 Sth132I
 MboII
 BcgI
 ApoI
 Tsp509I
 1201 CGCAAAATTTTGGTCAAAGGTAAGCAGCAAACTATCGAAGAAAATGCGTTATCAGGCGAC 1260
 -----+-----+-----+-----+-----+
 GCGTTTTAAACAGTTTCCATTTCGTCGTTGATAGCTTCTTTTACGCAATAGTCCGCTG

BccI
 CviJI
 AluI
 CviJI
 HhaI
 1261 CATCGGGCTTTTAGGAGCTTTGGCAATCATCTTGCTCTATGTGAGTTTGGCTTTGAATG 1320
 -----+-----+-----+-----+-----+
 GTAGCCCGAAAATCCTCGAAACCGTTAGTAGAACGAGATACACTCAAACGCGAACTTAC

NlaIII
 Hpy178III
 Tsp509I
 MseI
 BcefI
 MwoI
 TspRI
 MwoI
 HhaI
 RcaI
 CviJI
 MwoI
 CviRI
 1321 GCAATATGCTTTTCAGTGCCGTATGCGCTTTAATTCATGACCTTTTGGCTACCTGTGCAGT 1380
 -----+-----+-----+-----+-----+
 CGTTATACGAAAGTCACGGCATACGCGAAATTAAGTACTGGAAAACCGATGGACACGTCA

>SW:SECF_MYCTU Q50635 mycobacterium tuberculosis. protein-export membrane
protein secf. 11/97
Length = 442

Score = 90 (42.3 bits), Expect = 5.9e-16, Sum P(5) = 5.9e-16
Identities = 30/118 (25%), Positives = 50/118 (42%)

Query: 316 SEKIKIYFSDKALSYTKQIRASLLKLTIMSWRXCGIVVRNRPRFLYGNSKRNAKFWSKVS 375
SE + S T QIR+ L + + P+ G + A S VS
Sbjct: 121 SEPQSVVIVGAGASATVQIRSETLTSDQTAKLRDALFEAFGPKGTDGQPSKQAISDSAVS 180

Query: 376 SKLSKKMRYQATIGLLGALAIILLYVSLRFQYAFSAVCALIHDLATCAVLFIHF 433
++ +A I L+ L ++ LY+++R+E SA+ A++ DL T V + F
Sbjct: 181 ETWGGQITKKAVIALVFLVLVALYITVRYERYMTISAITAMLFDLTVTAGVYSLVGF 238